

Life Sciences Domain Analysis Model (LS DAM)

- Current Release
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Related Efforts

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Overview of the LS DAM

The caBIG Life Sciences Domain Analysis Model (LS DAM) is a shared view of the semantics for Life Sciences which includes hypothesis driven basic and pre-clinical research as well as discovery sciences. The LS DAM is a foundational component for achieving semantic interoperability among the various applications across caBIG.

This is a collaborative effort, currently engaging stakeholders from the National Cancer Institute (NCI), including the Cancer Biomedical Informatics Grid (caBIG) project, the HL7 Clinical Genomics Work Group (HL7 CG WG), and the Biomedical Research Integrated Domain Group (BRIDG).

The LS DAM is aligned, where appropriate, with the Biomedical Research Integrated Domain Group (BRIDG) model, which is a separate DAM that supports the domain of protocol driven clinical and pre-clinical research. The points of alignment highlight the touch points between life sciences and clinical research, and through these touch points, the two models can be used together to support semantic interoperability across the translational research continuum.

The intent is for the LS DAM to continue to evolve over time, becoming more refined and expanding to describe the full breadth of scope, as the model is used and the user community brings new concepts forward to be included.

The LS DAM is modeled in UML through Enterprise Architect. It is fully described through UML class and instance diagrams. The LS DAM is bound to the ISO 21090 data type standard.

Scope

Life Sciences research includes (i) *in vivo* experiments, (ii) *ex vivo*, *in vitro* or *in situ* experiments, and (iii) *in silico* experiments modeling and analyzing processes or other biological phenomena.

The Life Sciences Domain Analysis Model (LS DAM) focuses on concepts important for conducting hypothesis driven and discovery science at the organismal, cellular and molecular level. The LS DAM includes and defines relationships between concepts that are central to specimen collection, processing and banking (human, model organism, cell lines, etc.), *in vitro* imaging, and molecular biology.

LS DAM Context:

Concepts important to Clinical Research are contained in the BRIDG domain analysis model. The LS DAM and BRIDG models are harmonized on key concepts that can be used as touch points to allow utilization of elements from both models.

Release History

- LS DAM 2.2.1: May 2011
- LS DAM 2.2: April 2011
- LS DAM 2.1: February 2011
- LS DAM 2.0: October 2010
 - Alignment with BRIDG 3.0.2
 - Generic Assay model, developed in collaboration with the HL7 Clinical Genomics Work Group
- LS DAM 1.2: February 2010
 - includes extensions to provide a framework of support for the key concepts within the nano sub-domain
- LS DAM 1.1: October 2009
- LS DAM 1.0: July 2009
 - Initial release

Next Steps

Recommendations for future efforts on LS DAM include the following:

- Release under a two layer approach, providing a set of more domain-friendly top layer models that are generated from the complete model (the second layer)
- Further alignment with BRIDG
- Expansion of scope to better support:
 - Alignment with LS BAM
 - Organization- and Person-based roles not already included or supported in BRIDG
 - Examination of relationship between LS Protocol/Study/Experiment and BRIDG.StudyProtocol
 - Pathology Imaging
 - Specimen Distribution
 - Experimental design/outcome, Pathway/molecular interaction, Biomarkers

For more information on recommendations next steps, see the [Future Activities Compilation](#)

Current Team

Role	Name	Affiliation
ICR Workspace NCI Coordinator	Juli Klemm	NCI CBIIT
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IRWG	Grace Stafford	The Jackson Laboratory
IRWG	Baris Suzek	Georgetown University
LS DAM Analyst	Lisa Schick	ScenPro
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Using the LS DAM Wiki

This is the wiki home page of the LS DAM.